

# Phenotypic and genotypic analysis of a European winter wheat breeding panel for resistance to fusarium head blight (FHB)



Institute of  
Biotechnology in  
Plant Production,  
IFA Tulln

Anne-Laure Girard, supervisors : Laura Morales, Hermann Bürstmayr

Wheat is the second main source of calories worldwide and Fusarium head blight (FHB) is the second most problematic wheat pathogen. The use of conservation tillage (crop residues stay on the soil surface) can increase the survival of Fusarium spores but combined with disease resistant varieties it could increase wheat yield under sustainable agriculture practices. Although the most common approaches to reduce FHB rely on fungicide application and crop management, these techniques are not sufficient. Resistance breeding is therefore considered one of the most efficient, economic and environmentally friendly ways to control the disease. To find sources of resistance for FHB in cultivars adapted to European environments with good agronomic performance, a panel of European winter wheat breeding lines has been utilized to investigate the association between morphological traits and resistance to FHB.

## Fusarium head blight (FHB)

- Mainly caused by *F. graminearum* and *F. culmorum*
- Infection in wheat and other small grains
- Decreases wheat yield due to aborted and smaller kernels
- Production of mycotoxins dangerous to humans and livestock
- High correlation between FHB symptoms, damaged kernels, mycotoxin contamination and yield reduction
- High infection at anthesis under warm and humid weather



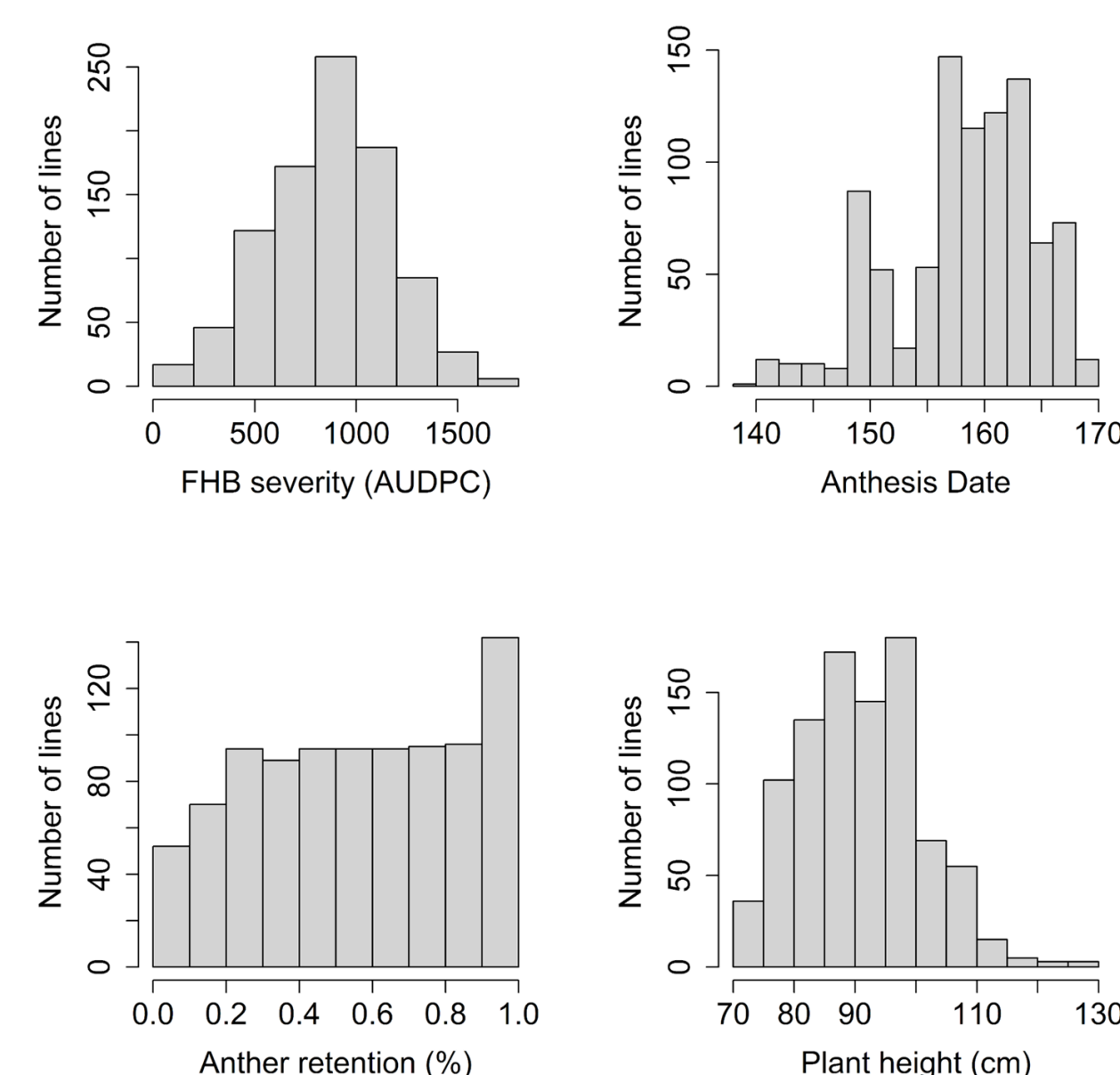
Symptoms of FHB on wheat heads

## Materials and methods

- 230 lines from Norway, Germany and Austria (training set from WheatSustain project)
- Planted in two years with two replications per year in Tulln, Austria
- Completely randomized block design
- Inoculated with *F. culmorum* throughout anthesis period

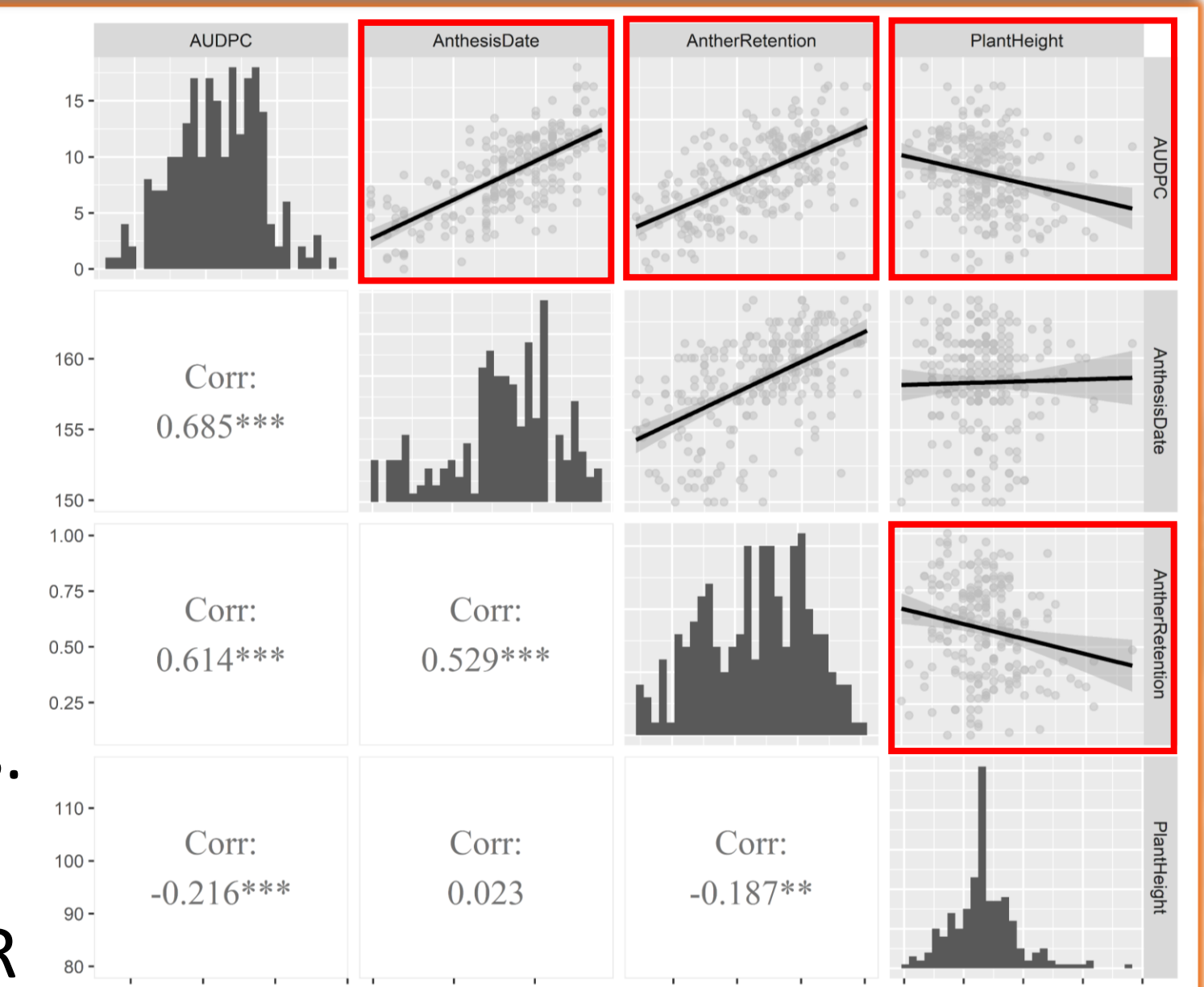
## Traits measured and phenotypic distribution

- 920 observations
- Anthesis date (AD) -> day in the year
- Anther retention (AR) -> percentage
- Plant height (PH) -> cm
- FHB severity
  - visual damage on wheat head
  - > Area under disease progress curve (AUDPC)
  - 10, 14, 18, 22, 26, 30 days after inoculation



## Genotypic correlations between traits

- **FHB resistance** was associated with:
  - **Early AD:** weather conditions at anthesis may have influenced FHB symptom development.
  - **Low AR:** AR increases initial infection.
  - **Increased PH:** due to differences in the microclimate around spikes. Dwarfing alleles decrease PH, but also increase the proportion of AR due to stiffer glumes and shorter filaments, which can increase FHB severity.



Genotypic correlations (based on genotype best linear unbiased predictors for each trait) with scatter plots and regression lines of traits assessed in 2020 and 2021. Significance levels: \* p-value < 0.05, \*\* p-value < 0.01, \*\*\* p-value < 0.001

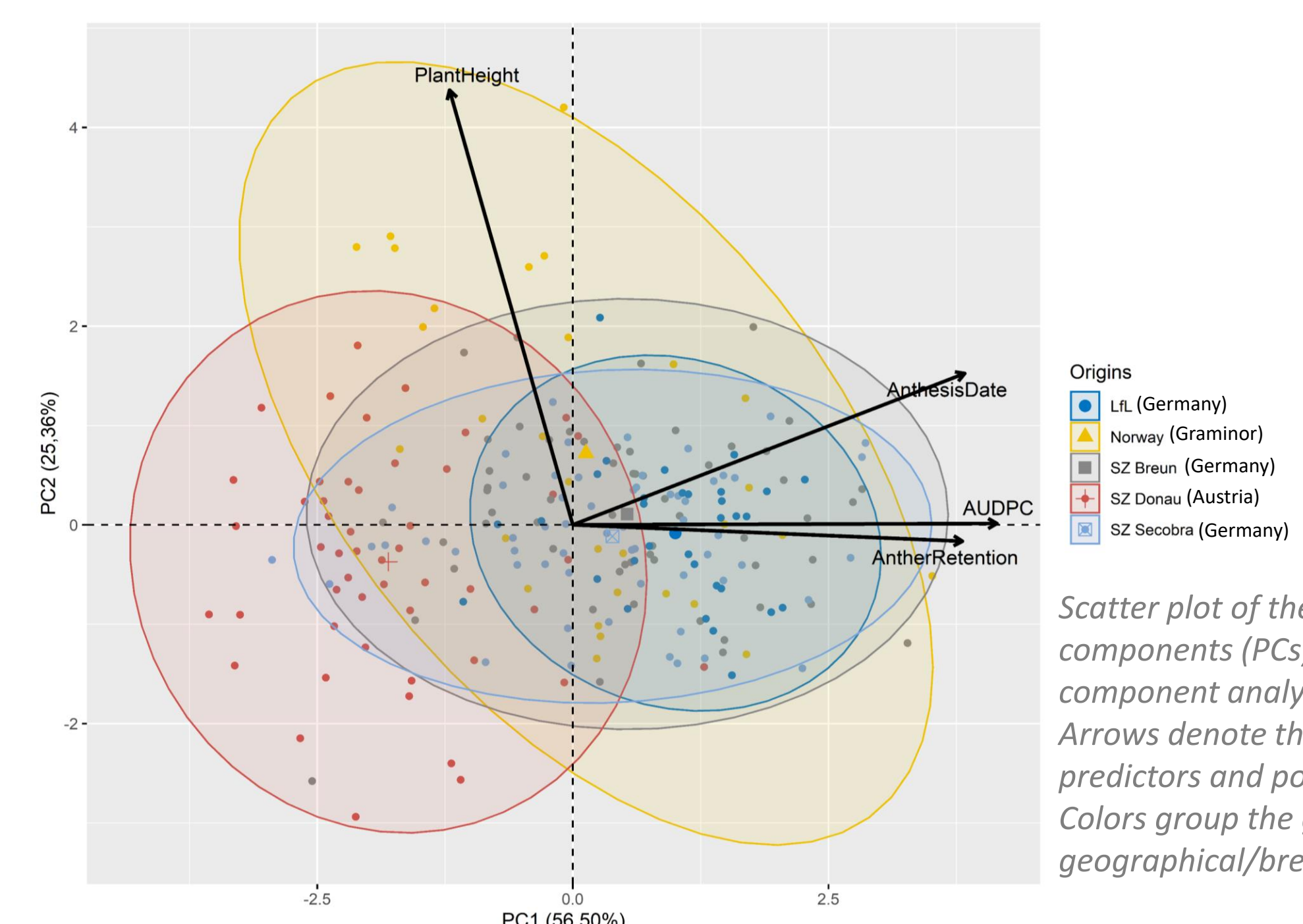
## Heritability and variance components

	AUDPC FHB severity	Anthesis date	Anther retention	Plant height
$\sigma^2_{\text{Genotype}}$	0,43	0,18	0,30	0,17
$\sigma^2_{\text{Year}}$	0,00	0,63	0,17	0,70
$\sigma^2_{\text{Replicate[Year]}}$	0,12	0,13	0,00	0,00
$\sigma^2_{\text{Genotype*Year}}$	0,21	0,02	0,22	0,06
$\sigma^2_{\text{Error}}$	0,24	0,04	0,32	0,07
<b>Heritability</b>	<b>0,73</b>	<b>0,91</b>	<b>0,61</b>	<b>0,78</b>

Proportion of the total variance explained by genetic and environmental terms ( $\sigma^2$ ) and heritability for FHB severity, anthesis date, anther retention and plant height.  $\sigma^2_{\text{Genotype}}$ : genotypic variance,  $\sigma^2_{\text{Year}}$ : variance of year,  $\sigma^2_{\text{Replicate[Year]}}$ : variance of the replicate nested in year,  $\sigma^2_{\text{Genotype*Year}}$ : variance of the genotype by year interaction,  $\sigma^2_{\text{Error}}$ : residual variance.

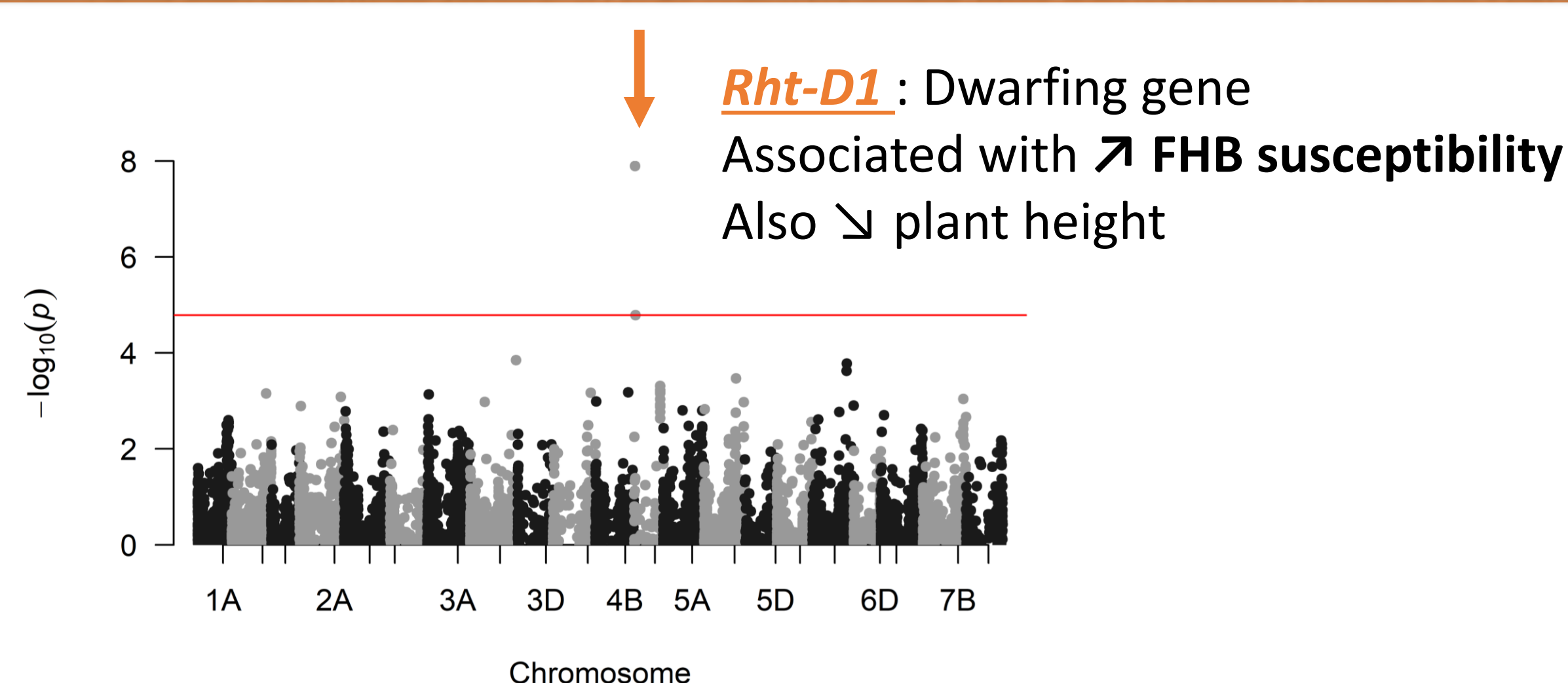
- FHB was highly heritable but can be difficult to assess under field conditions as symptom development is influenced by environmental conditions.
- All traits were highly heritable.
- AR was influenced by dry and warm conditions at anthesis.
- AD and PH were strongly influenced by the environment.

## Origins of the plant material



- Differences in the population are mainly driven by FHB severity and AR.
- The Austrian material differed from the rest with lower FHB severity and shorter AD while the Norwegian material was taller than the other lines.
- Lines from the same country clustered together which demonstrated a common genetic background.

## Genome wide association



Manhattan plot showing the significant SNP associated with FHB susceptibility. Data from other locations has also been used.

- The *Rht-D1* semi-dwarfing gene is significantly associated with FHB severity.
- The introgression of resistance loci is one strategy for developing resistant lines.

## Conclusion

- **Low AR** (or high anther extrusion) can be used for **indirect selection of passive resistance mechanisms** as AR does not have a negative impact on agronomic performance.
- **High anther extrusion** can **limit the initial infection** but cannot provide complete protection against FHB.
- **Correcting FHB scores** with associated traits can **improve physiological resistance**.
- **AD and PH** need to be considered to **avoid negative trade-offs**:
  - early AD -> wheat sterility, poor adaptation
  - high PH -> lodging
- Loci associated with FHB can be used in selection.

### References:

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 -STEINER Barbara, BUERSTMAYR Maria, WAGNER Christian, DANLER Andrea, ESHONKULOV Babur, EHN Magdalena and BUERSTMAYR Hermann, 2019. Fine-mapping of the Fusarium head blight resistance QTL Qfhs.ifa-5A identifies two resistance QTL associated with anther extrusion. *Theoretical and Applied Genetics*. 1 July 2019. Vol. 132, no. 7, p. 2039–2053. DOI 10.1007/s00122-019-03336-x.  
 -COOK R. James, 2006. Toward cropping systems that enhance productivity and sustainability. *Proceedings of the National Academy of Sciences*. 5 December 2006. Vol. 103, no. 49, p. 18389–18394. DOI 10.1073/pnas.0605946103.